

**Amendments to the Specification:**

A. Please replace the fifth full paragraph on page 5, with the following amended paragraph:  
FIGS. 5.1 to 5.46 present the coordinates for the crystal structure of Aequorea-related green fluorescent protein S65T (~~SEQ ID NOS:5,6~~) (SEQ ID NO:5).

B. Please replace Table B which starts at line 24 on page 30, with the following amended table:

TABLE B

	Original position and presumed role	Change to	Codon
L42	Aliphatic residue near C=N of chromophore	C, E, H, I, Q, R, W, Y, Z ( <del>SEQ ID NO:7</del> )	5'YDS 3' 3'RHS 5'
V61	Aliphatic residue near central —CH= of chromophore	F, Y, H, C, L, R ( <del>SEQ ID NO:8</del> )	YDC RHg
T62	Almost directly above center of chromophore bridge	A, V, F, S, ( <del>SEQ ID NO:9</del> )  D, E, H, K, N, Q ( <del>SEQ ID NO:10</del> )  F, Y, H, C, L, R ( <del>SEQ ID NO:8</del> )	KYC MRg VAS BTS YDC RHg
V68	Aliphatic residue near carbonyl and G67	F, Y, H, L ( <del>SEQ ID NO:11</del> )	YWC RWg
N121	Near C—N site of ring closure between T65 and G67	C, E, H, I, Q, R, W, Y, Z ( <del>SEQ ID NO:7</del> )	YDS RHS
Y145	Packs near tyrosine ring of chromophore	W, C, F, L ( <del>SEQ ID NO:12</del> )  D, E, H, N, K, Q ( <del>SEQ ID NO:13</del> )	TKS AMS VAS BTS
H148	H-bonds to phenolate oxygen	F, Y, N, I ( <del>SEQ ID NO:14</del> )  K, Q, R	WWC WWg MRg KYC
V150	Aliphatic residue near tyrosine ring of chromophore	F, Y, H, L ( <del>SEQ ID NO:11</del> )	YWC RWg
F165	Packs near tyrosine ring	C, H, Q, R, W, Y, Z ( <del>SEQ ID NO:15</del> )	YRS RYS
I167	Aliphatic residue near phenolate; I167T has effects	F, Y, H, L ( <del>SEQ ID NO:11</del> )	YWC RWg
T203	H-bonds to phenolic oxygen of chromophore	F, H, I, Q, R, W, Y, Z ( <del>SEQ ID NO:16</del> )	YDS RHS
E222	Protonation regulates ionization of	H, K, N, Q ( <del>SEQ ID</del> )	MAS

	chromophore	<b>NO:17)</b>	KTS
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C. Please replace Table C which starts at line 1 page 32 with the following amended table:

TABLE C

	Original position and presumed role	Change to	Codon
Q69	Terminates chain of H-bonding waters	<b>K, R, E, G (SEQ ID NO:18)</b>	RRg YYC
Q94	H-bonds to carbonyl terminus of chromophore	<b>D, E, H, K, N, Q (SEQ ID NO:10)</b>	VAS BTS
Q183	Bridges Arg96 and center of chromophore bridge	<b>H, Y</b> <b>E, K</b>	YAC RTG RAG YTC
N185	Part of H-bond network near carbonyl of chromophore	<b>D, E, H, N, K, Q (SEQ ID NO:13)</b>	VAS BTS

D. Please replace Table D, which starts at line26, page 32, with the following amended table:

TABLE D

	Original position and presumed role	Change to	Codon
L220	Packs next to Glu222; to make GFP pH sensitive	<b>H, K, N, P, Q, T (SEQ ID NO:19)</b>	MMS KKS
V224	Packs next to Glu222; to make GFP pH sensitive	<b>H, K, N, P, Q, T (SEQ ID NO:19)</b> <b>C, F, H, L, Q, R, W, Y, Z (SEQ ID NO:7)</b>	MMS KKS YDS RHS